ISSN (e): 2250 – 3005 || Volume, 05 || Issue, 03 || March – 2015 ||
International Journal of Computational Engineering Research (IJCER)

Qualitative Analysis of a Discrete SIR Epidemic Model

A. George Maria Selvam [1], D. Jerald Praveen [2]
[1, 2] Sacred Heart College, Tirupattur - 635 601, S.India

ABSTRACT:
The dynamical behaviors of a discrete-time SIR epidemic model are analyzed in this paper. Existence and stability of disease-free and endemic equilibria are investigated. Basic reproduction number for the system is computed. Numerical simulations show that the system has complex and rich dynamics and can exhibit complex patterns, depending on the parameters. Also the bifurcation diagrams are presented.
KEYWORDS: *Epidemic model, difference equations, stability, bifurcation.*

I. INTRODUCTION

Infectious diseases have tremendous influence on human life. Every year millions of human beings suffer or die of various infectious diseases. Controlling infectious diseases has been an increasingly complex issue in recent years. Mathematical models have been extensively used in the study of spread of epidemics and diseases. The models aim to capture the major factors that are responsible for the progression of diseases, and can forecast how diseases spread. The results obtained from these models are useful in predicting how infectious diseases develop and spread. Kermack and McKendrick derived the simple classical SIR model in 1927. In the classical epidemiological SIR model, a population of total size N is divided into S susceptible numbers, I infective numbers, and R recovered numbers.

II. FORMATTING YOUR PAPER

Analytical and numerical studies of system of difference equations models in epidemiology have uncovered a number of interesting dynamical behaviors including stable steady states, oscillation, limit cycles and chaos. In recent years, several authors formulated and studied natural discrete approximation to the continuous epidemic models obtained by applying Euler's Method. In this paper, we consider the SIR epidemic model as a system of difference equations. In this model, the susceptible host population is assumed to follow the logistic growth with a specific growth rate constant r. The force of infection is $\frac{\beta S(n)I(n)}{1+aS(n)}$. The parameter a measures the inhibitory effect, γ is the natural recovery rate of the infective individuals. Also μ and λ represent the per capita death rates of infective and recovered. Throughout this paper, we assume $a \neq 0$.

$$\begin{aligned} S(n+1) &= rS(n)[1-S(n)] - \frac{\beta S(n)I(n)}{1+aS(n)} \\ I(n+1) &= \frac{\beta S(n)I(n)}{1+aS(n)} + (1-(\mu+\gamma))I(n) \\ R(n+1) &= \gamma I(n) + (1-\lambda)R(n) \end{aligned} \qquad (1)$$

We restrict our attention to the reduced model described by the system of following two equations.

$$\begin{aligned} S(n+1) &= rS(n)[1-S(n)] - \frac{\beta S(n)I(n)}{1+aS(n)} \\ I(n+1) &= \frac{\beta S(n)I(n)}{1+aS(n)} + (1-(\mu+\gamma))I(n) \end{aligned} \qquad (2)$$

A point x^* is said to be a fixed point (or equilibrium point) of a map f if $f(x^*) = x^*$. It is important to develop qualitative or graphical methods to determine the behavior of the orbits near fixed points. We consider the equilibria of system. The system admits the Equilibrium points $E_0 = \left(\frac{r-1}{r}, 0\right)$ (the disease free equilibrium since I and R components are zero), $E_1 = \left(\frac{K}{A}, \frac{1+r}{A} - \frac{rK}{A^2}\right)$ where $K = \mu + \gamma$ and $A = -\beta + a\mu + a\gamma$, (endemic equilibrium of the model).

III. DYNAMIC BEHAVIOR OF THE MODEL

The purpose of this paper is to study the nonlinear dynamics of system. Mathematically, the stability of the equilibrium points starts with linearization of the system (1). The stability of these equilibrium points can be investigated by linearization. The Jacobian Matrix for the reduced system (2) is

$$J(S,I,R)=\begin{bmatrix} r-2rS-\frac{(1+aS)\beta I-\beta SIa}{(1+aS)^2} & -\frac{\beta S}{1+aS} \\ \frac{(1+aS)\beta I-\beta SIa}{(1+aS)^2} & \frac{\beta S}{1+aS}+(1-K) \end{bmatrix} \qquad (3)$$

Trace $J(S,I,R)=r-2rS-\frac{(1+aS)\beta I-\beta SIa}{(1+aS)^2}+\frac{\beta S}{1+aS}+(1-K)$ and

Det $J(S,I,R)=\left(r-2rS-\frac{(1+aS)\beta I-\beta SIa}{(1+aS)^2}\right)\left(\frac{\beta S}{1+aS}+(1-K)\right)+\left(\frac{(1+aS)\beta I-\beta SIa}{(1+aS)^2}\right)\left(\frac{\beta S}{1+aS}\right)$

Lemma 1. Let

$$p(\lambda)=\lambda^2+p_1\lambda+p_2=0 \qquad (4)$$

be the characteristic equation for a matrix defined by (3). Then the following statements are true:

- If every root of equation (4) has absolute value less than one, then the equilibrium point of the system (1) is locally asymptotically stable and equilibrium point is called a sink.
- If every root of equation (4) has absolute value greater than one, then the equilibrium point of the system (1) is a source.
- The equilibrium point of system (1) is called hyperbolic if no root of equation (4) has absolute value equal to one. If there exists a root of equation (4) with absolute value equal to one, then the equilibrium point is called non-hyperbolic.

Proposition 2. The disease free equilibrium point E_0 is a

Sink if $1<r<3$ and $-\left(\frac{2-K(r+a(r-1))}{r-1}\right)<\beta<\frac{K(r+a(r-1))}{r-1}$

Source if $r>3$ and $\frac{\beta(r-1)}{r+a(r-1)}-\gamma>\mu>2+\frac{\beta(r-1)}{r+a(r-1)}-\gamma$

Non hyperbolic if $r=1$ and $\frac{K(r+a(r-1))}{r-1}$

Proof:

$$J(E_0)=\begin{bmatrix} -r+2 & -\frac{\beta(r-1)}{r+a(r-1)} \\ 0 & \frac{\beta(r-1)}{r+a(r-1)}+(1-K) \end{bmatrix} \qquad (5)$$

The Eigen values of the matrix $J(E_0)$ are $\lambda_1=-r+2$, $\lambda_2=\frac{\beta(r-1)}{r+a(r-1)}+(1-K)$. In view of Lemma, we see that, E_0 is a sink if $1<r<3$ and $-\left(\frac{2-K(r+a(r-1))}{r-1}\right)<\beta<\frac{K(r+a(r-1))}{r-1}$. E_0 is a source if $r>3$ and $\frac{\beta(r-1)}{r+a(r-1)}-\gamma>\mu>2+\frac{\beta(r-1)}{r+a(r-1)}-\gamma$. Also E_0 is non-hyperbolic if $r=1$ and $\frac{K(r+a(r-1))}{r-1}$.

The basic reproduction number R_0 is defined as the average number of secondary infections that occur when one infective is introduced into a completely susceptible host population. R_0 is also called the basic reproduction ratio or basic reproductive rate. For our system $R_0=\frac{\beta(r-1)}{(r+a(r-1))(\mu+\gamma)}$ is the reproduction number.

$$J(E_1)=\begin{bmatrix} r-\frac{2rK}{A}-\frac{\beta K\left(1+r-\frac{rK}{A}\right)(1+a)}{(A+aK)^2} & \frac{-\beta K}{A+aK} \\ \frac{\beta K\left(1+r-\frac{rK}{A}\right)(1+a)}{(A+aK)^2} & \frac{\beta K}{A+aK}(1-K) \end{bmatrix} \qquad (6)$$

Trace $J(E_1)=p_1=r-\frac{2rK}{A}-\frac{\beta K\left(1+r-\frac{rK}{A}\right)(1+a)}{(A+aK)^2}+\frac{-\beta K}{A+aK}(1-K)$

$$\text{Det } J(E_1) = p_1 = \left(r - \frac{2rK}{A} - \frac{\beta K\left(1 + r - \frac{rK}{A}\right)(1 + a)}{(A + aK)^2}\right)\left(\frac{\beta K}{A + aK}(1 - K)\right)$$
$$- \left(\frac{\beta K\left(1 + r - \frac{rK}{A}\right)(1 + a)}{(A + aK)^2}\right)\left(\frac{\beta K}{A + aK}\right)$$

IV. NUMERICAL EXAMPLES

In this section, we present some numerical simulations of system (1) to illustrate our results. The numerical examples substantiate the analytical results obtained in the previous section. Numerical study of nonlinear discrete dynamical systems gives an insight in to dynamical characteristics. The time plots for S(n); I(n); R(n), phase portraits and bifurcation diagrams for the system (1) are presented. Dynamic behaviors of the system (1) about the equilibrium points under different sets of parameter values are studied.

Example 1. Take $r = 2.95, \beta = 0.8, \gamma = 0.15, \mu = 0.00999.$

Since R_0 then the disease-free equlibrium is globally asymptotically stable for any period.

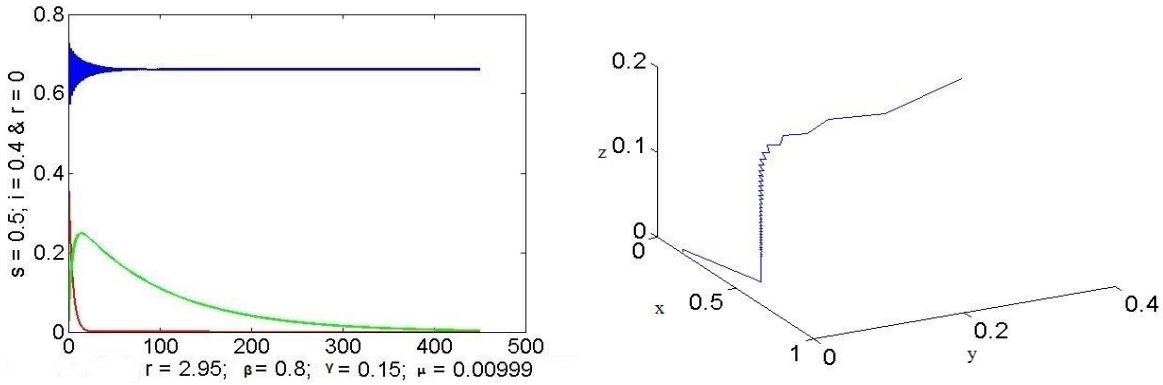

Figure 1. Dynamical Behavior of Trivial Equilibrium points $R_0 < 1$

Example 2. Take $r = 2.7, \beta = 0.35, \gamma = 0.059, \mu = 0.00999.$

Since $R_0 > 1$ then the endemic equilibrium is globally asymptotically stable for any period.

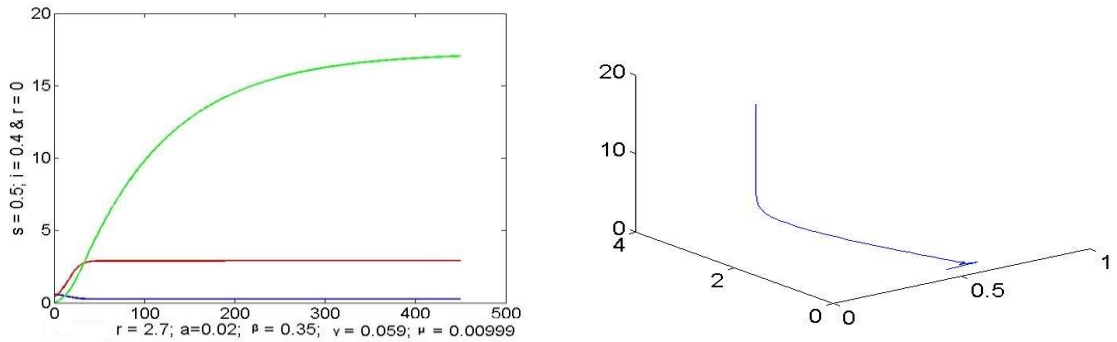

Figure 2. Dynamical Behavior of Trivial Equilibrium points $R_0 > 1$

Example 3. Take $r = 2.95, \beta = 1.7, \gamma = 0.15, \mu = 0.00999$. The system exhibits oscillatory behaviour and the phase portrait is reduced to a limit cycle.

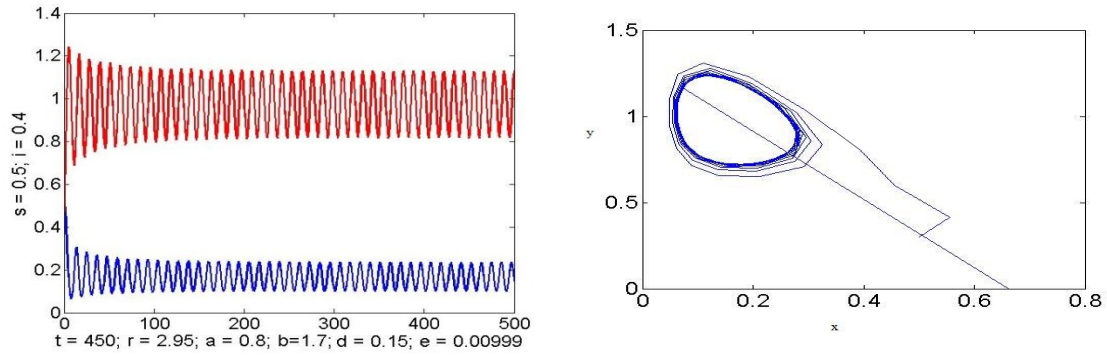

Figure 3. Time plot of Interior Equilibrium Point

Example 4. Take $a = 0.8, r = 2.95, \mu = 0.009, \gamma = 0.05, \lambda = 0.0099$. Also β is given three different values $\beta = 0.097, 0.068, 0.19$ together with the other parameter such that $R_0 < 1$. The infection dynamics is illustrated in the Figure-4.

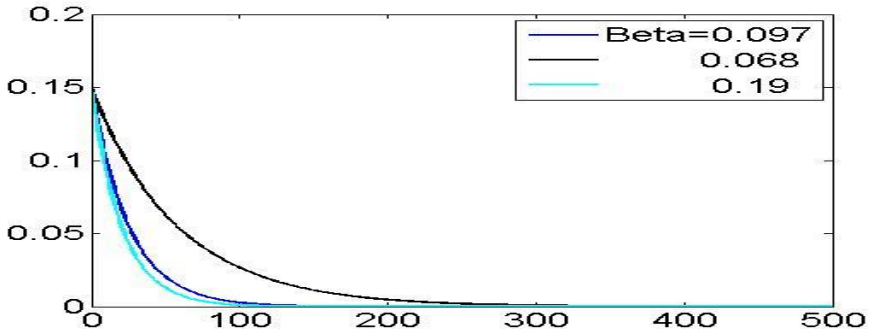

Figure 4. variation of Beta

V. BIFURCATION

Bifurcation theory is the mathematical study of changes in the qualitative behavior of a given family and the solutions of a family of differential equations. Most commonly applied to the mathematical study of dynamical systems, a bifurcation occurs when a small smooth change made to the parameter values (the bifurcation parameters) of a system causes a sudden 'qualitative' or topological change in its behaviour. In general, the term bifurcation refers to the phenomenon of a system exhibiting new dynamical behavior as a parameter is varied. The numerical analysis of bifurcation problems is concerned with the stable, reliable and efficient computation of solutions to nonlinear problems. The technique of linearization used for stability analysis may fail at bifurcation points, for near such points the dynamical behaviors of the system may differ qualitatively from those of its linearized system. The Neimark Saker bifurcation for discrete dynamical systems corresponds to the Hopf bifurcation in the continuous case. We use the numerical simulations to display bifurcation diagram for susceptible population.

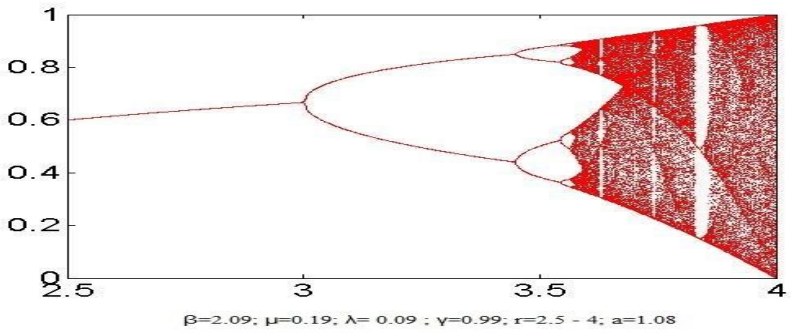

Figure 5. Bifurication

The following diagrams exhibit the change in the dynamical nature of $S(n)$ for values of r chosen from different ranges in the bifurcation diagram.

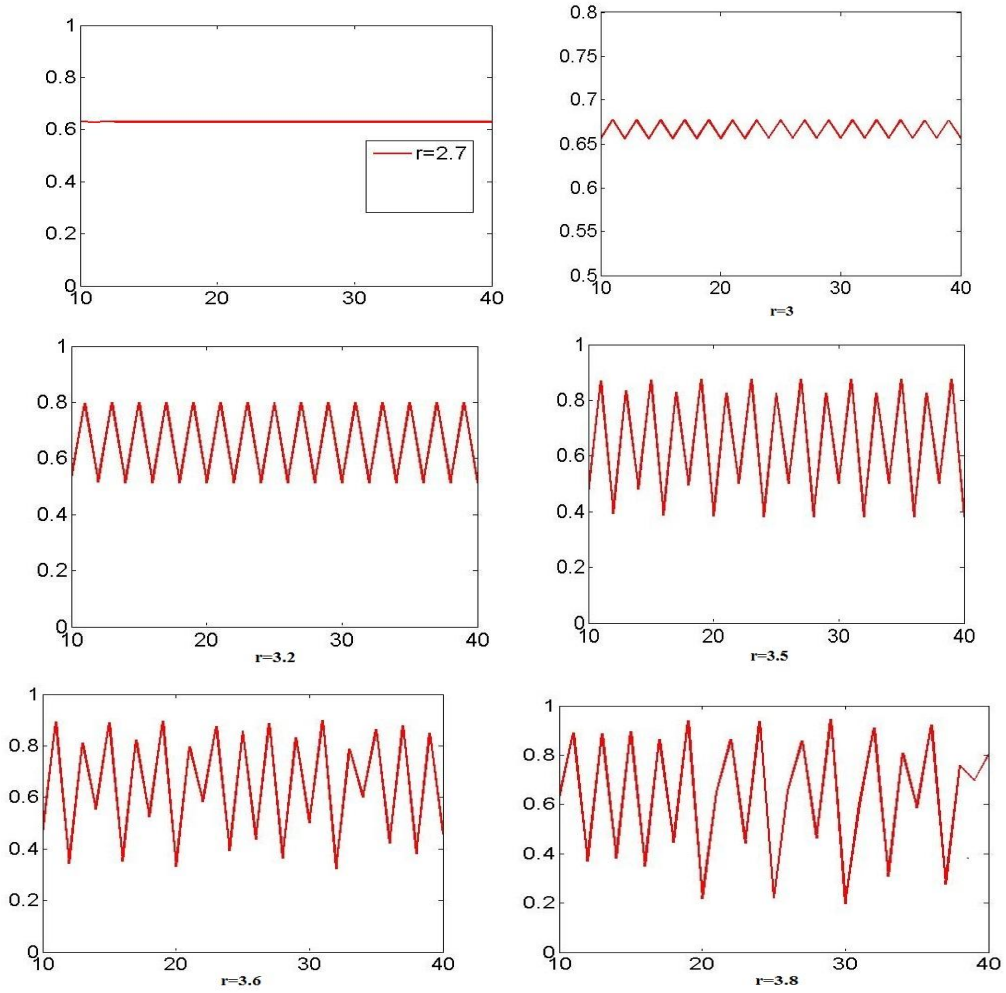

Figure 6. Dynamics in different values of r

In the present paper we examined the bifurcation of a mathematical model for the spread of an infectious disease. In order to eradicate the disease, the basic reproduction number R_0 must be lowered than a threshold. The basic reproductive number R0 determines the existence of the equilibrium. When $R_0 \leq 1$, model (1) has a unique disease-free equilibrium. When $R_0 > 1$, model (1) has a disease-free equilibrium and a unique endemic equilibrium.

REFERENCES

[1] Anderson, R. M. and May, R. M. (1986). The invasion, persistence, and spread of infectious diseases within animal and plant communities, Philos Trans R Soc Lond B 314: 533-570.
[2] Jacek Banasiak, Modelling with Difference and Differential Equations, Cambridge University Press.
[3] Kang-Hung Yang, Jin-Yuan Hsu, A New SIR-based Model for Influenza Epidemic, World Academy of Science, Engineering and Technology Vol:6 2012-07-20.
[4] Kermack, W. O. McKendrick, A. G. (1927). "A Contribution to the Mathematical Theory of Epidemics". Proceedings of the Royal Society A: Mathematical, Physical and Engineering Sciences 115 (772): 700. doi:10.1098/rspa.1927.0118. JSTOR 94815.
[5] Leah Edelstein-Keshet, Mathematical Models in Biology, SIAM, Random House, New York, 2005.
[6] R. M. May, R. M. Anderson, and A. R. McLean, Possible demographic consequences of HIV/AIDS, Math. Biosci., 90 (1988), pp.475-506.
[7] A. G. McKendrick, Applications of mathematics to medical problems, Proc. Edinburgh Math. Soc., 44(1926), pp.98-130.
[8] J.D. Murray, Mathematical Biology I: An Introduction, 3-e, Springer International Edition, 2004.
[9] Saber Elaydi, An Introduction to Difference Equations, Third Edition, Springer International Edition, First Indian Reprint, 2008.
[10] Xinzhu Meng and Lansun Chen, GLOBAL DYNAMICAL BEHAVIORS FOR AN SIR EPIDEMIC MODEL WITH TIME DELAY AND PULSE VACCINATION, TAIWANESE JOURNAL OF MATHEMATICS Vol. 12, No. 5, pp. 1107-1122, August 2008.
[11] Zhixing Hu, Wanbiao Ma, Shigui Ruan, Analysis of SIR epidemic models with nonlinear incidence rate and treatment, Mathematical Biosciences 238 (2012) 12–20.